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SEQUENCE LISTING

<110> TWINSTRAND THERAPEUTICS INC. BORGFORD, Thor BRAUN, Curtis PURAC, Admir STOLL, Dominik <120> GLYCOSYLATION VARIANTS OF RICIN-LIKE PROTEINS <130> 10447-42 <140> <141> <150> US 60/555,678 <151> 2004-03-24 <160> 6 <170> PatentIn version 3.3 <210> 1 <211> 530 <212> PRT <213> Artificial Sequence <220> <223> TST10088 Protein Sequence <400> 1 Glu Ala Glu Ala Ile Phe Pro Lys Gln Tyr Pro Ile Ile Gln Phe Thr 10 Thr Ala Gly Ala Thr Val Gln Ser Tyr Thr Asn Phe Ile Arg Ala Val 25 Arg Gly Arg Leu Thr Thr Gly Ala Asp Val Arg His Glu Ile Pro Val Leu Pro Asn Arg Val Gly Leu Pro Ile Asn Gln Arg Phe Ile Leu Val 55 Glu Leu Ser Asn His Ala Glu Leu Ser Val Thr Leu Ala Leu Asp Val 75 Thr Asn Ala Tyr Val Val Gly Tyr Arg Ala Gly Asn Ser Ala Tyr Phe 90 Phe His Pro Asp Asn Gln Glu Asp Ala Glu Ala Ile Thr His Leu Phe 100 105

Thr Asp Val Gln Asn Arg Tyr Thr Phe Ala Phe Gly Gly Asn Tyr Asp

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Gly	Gly	Thr	Gln	Leu 165	Pro	Thr	Leu	Ala	Arg 170	Ser	Phe	Ile	Ile	Cys 175	Ile
Gln	Met	Ile	Ser 180	Glu	Ala	Ala	Arg	Phe 185	Gln	Tyr	Ile	Glu	Gly 190	Glu	Met
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Gly	Ser	Lys	Phe	Ser 245	Val	туг	Asp	Val	Ser 250	Ile	Leu	Ile	Pro	Ile 255	Ile
Ala	Leu	Met	Val 260	Tyr	Arg	Cys	Ser	Pro 265	Gln	Gly	Ile	Ala	Gly 270	Gln	Cys
Met	Asp	Pro 275	Glu	Pro	Ile	Val	Arg 280	Ile	Val	Gly	Arg	Asn 285	Gly	Leu	Cys
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Arg	Asp	Asn	Thr	Ile 325	Arg	Ser	Asn	Gly	Lys 330	Cys	Leu	Thr	Thr	Tyr 335	Gly
Tyr	Ser	Pro	Gly 340	Val.	Tyr	Val	Met	Ile 345	Tyr	Asp	Cys	Asn	Thr 350	Ala	Ala
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Pro Arg Ser Ser Leu Val Leu Ala Ala Thr Ser Gly Asn Ser Gly Thr 370 380

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Pro Thr Gln Asn Thr Gln Pro Phe Val Thr Thr Ile Val Gly Leu Tyr
405 410 415

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Ser Ser Glu Lys Ala Glu Gln Gln Trp Ala Leu Tyr Ala Asp Gly Ser 435 440 445

Ile Arg Pro Gln Gln Asn Arg Asp Asn Cys Leu Thr Ser Asp Ser Asn 450 455 460

Ile Arg Glu Thr Val Val Lys Ile Leu Ser Cys Gly Pro Ala Ser Ser 465 470 475 480

Gly Gln Arg Trp Met Phe Lys Asn Asp Gly Thr Ile Leu Asn Leu Tyr 485 490 495

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Met Asp Pro Glu Pro Ile Val Arg Ile Val Gly Arg Asn Gly Leu Cys 280 Val Asp Val Arg Asp Gly Arg Phe His Asn Gly Asn Ala Ile Gln Leu 300 Trp Pro Cys Lys Ser Asn Thr Asp Ala Asn Gln Leu Trp Thr Leu Lys 310 315 Arg Asp Asn Thr Ile Arg Ser Asn Gly Lys Cys Leu Thr Thr Tyr Gly 330 Tyr Ser Pro Gly Val Tyr Val Met Ile Tyr Asp Cys Asn Thr Ala Ala 340 345 Thr Asp Ala Thr Arg Trp Gln Ile Trp Asp Asn Gly Thr Ile Ile Asn 355 360 365 Pro Arg Ser Ser Leu Val Leu Ala Ala Thr Ser Gly Asn Ser Gly Thr 370 375 380 Thr Leu Thr Val Gln Thr Asn Ile Tyr Ala Val Ser Gln Gly Trp Leu 390 Pro Thr Asn Asn Thr Gln Pro Phe Val Thr Thr Ile Val Gly Leu Tyr 405 410 Gly Leu Cys Leu Gln Ala Asn Ser Gly Gln Val Trp Ile Glu Asp Cys 420 425 Ser Ser Glu Lys Ala Glu Gln Gln Trp Ala Leu Tyr Ala Asp Gly Ser Ile Arg Pro Gln Gln Asn Arg Asp Asn Cys Leu Thr Ser Asp Ser Asn Ile Arg Glu Thr Val Val Lys Ile Leu Ser Cys Gly Pro Ala Ser Ser 470 475 Gly Gln Arg Trp Met Phe Lys Asn Asp Gly Thr Ile Leu Asn Leu Tyr 485 490 Ser Gly Leu Val Leu Asp Val Arg Ala Ser Asp Pro Ser Leu Lys Gln 505

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Leu Phe 530

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Leu Pro Asn Arg Val Gly Leu Pro Ile Asn Gln Arg Phe Ile Leu Val 50 55

Glu Leu Ser Asn His Ala Glu Leu Ser Val Thr Leu Ala Leu Asp Val 70 75

Thr Asn Ala Tyr Val Val Gly Tyr Arg Ala Gly Asn Ser Ala Tyr Phe 95

Phe His Pro Asp Asn Gln Glu Asp Ala Glu Ala Ile Thr His Leu Phe 100

Thr Asp Val Gln Asn Arg Tyr Thr Phe Ala Phe Gly Gly Asn Tyr Asp 115 120

Arg Leu Glu Gln Leu Ala Gly Asn Leu Arg Glu Asn Ile Glu Leu Gly 130 135 140

Asn Gly Pro Leu Glu Glu Ala Ile Ser Ala Leu Tyr Tyr Tyr Ser Thr 145 160

Gly Gly Thr Gln Leu Pro Thr Leu Ala Arg Ser Phe Ile Ile Cys Ile 165 170

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PCT/CA2005/000436

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Tyr Gly Leu Cys Leu Gln Ala Asn Ser Gly Gln Val Trp Ile Glu Asp 420 Cys Ser Ser Glu Lys Ala Glu Gln Gln Trp Ala Leu Tyr Ala Asp Gly 435 440 Ser Ile Arg Pro Gln Gln Asn Arg Asp Asn Cys Leu Thr Ser Asp Ser 450 455 460 Asn Ile Arg Glu Thr Val Val Lys Ile Leu Ser Cys Gly Pro Ala Ser 465 470 475 480 Ser Gly Gln Arg Trp Met Phe Lys Asn Asp Gly Thr Ile Leu Asn Leu 485 490 Tyr Ser Gly Leu Val Leu Asp Val Arg Ala Ser Asp Pro Ser Leu Lys 500 505 Gln Ile Ile Leu Tyr Pro Leu His Gly Asp Pro Asn Gln Ile Trp Leu 515 520 525 Pro Leu Phe 530 <210> 4 <211> 1707 <212> DNA <213> Artificial Sequence <220> <223> TST10088 DNA Insert Sequence <220> <221> prim_transcript <222> (1)..(117) atgaaaccgg gaggaaatac tattgtaata tgggtgtatg cagtggcaac atggctttgt 60 tttggatcca cctcagggtg gtctttcaca ttagaggata acaacctcga gaaaagagag 120 gctgaagcta tattccccaa acaataccca attatacagt ttaccacagc gggtgccact 180 gtgcaaagct acacaaactt tatcagagct gttcgcggtc gtttaacaac tqqaqctgat 240 gtgagacatg aaataccagt gttgccaaac agagttggtt tgcctataaa ccaacggttt 300 attttagttg aactctcaaa tcatgcagag ctttctgtta cattagcgct ggatgtcacc 360 aatgcatatg tggtcggcta ccgtgctgga aatagcgcat atttctttca tcctgacaat 420

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